## STIC Biotechnology Systems Branch

## RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number:

Source:

Date Processed by STIC:

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

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http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<a href="http://www.uspto.gov/ebc/efs/downloads/documents.htm">http://www.uspto.gov/ebc/efs/downloads/documents.htm</a>, EFS Submission User Manual ePAVE)
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building. 401 Dulany Street. Alexandria. VA 22314

Revised 01/24/05



PCT

RAW SEQUENCE LISTING DATE: 02/02/2005 PATENT APPLICATION: US/10/522,106 TIME: 15:31:41

```
2 <110 > APPLICANT: Kogel, Karl-Heinz
       3
               Huckelhoven, Ralph
               Trujillo, Marco
       6 <120> TITLE OF INVENTION: Method for Obtaining a Pathogen Resistance in Plants
       8 <130> FILE REFERENCE: 532622010500
                                                    15 lx pain Does Not Comply
15 lx pain Does Not Comply
Corrected Diskette Needed
(P5.1,3)

La See erronexplanation
Took page 5.
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/522,106
      11 <141> CURRENT FILING DATE: 2005-01-24
      13 <160> NUMBER OF SEQ ID NOS: 24
      14 <170> SOFTWARE: PatentIn Ver. 2.1
ERRORED SEQUENCES
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      46 <211> LENGTH: 112
      47 <212> TYPE: PRT
      48 <213> ORGANISM: Hordeum vulgare
 W--> 49 <400> SEQUENCE: 2
      50 Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile 🔿 🏷
                                                10
      52 Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
                       20
      54 Arg Ser Ala Leu Ile Thr Met/Leu Gln Ala Leu Asn His Ala Lys Asn
                  35
                                      /40
 E--> 56 Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
              50
      58 Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
                                70
      60 Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
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                                           105
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      2187 1
                               5
      2188 Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser Gly Pro Leu
                        20
                                               25
      2190 Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala Arg Phe Asn
                     35
      2191
```

### RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005 TIME: 15:31:42

2192 2193	Ile	Pro 50	Glu	Ser	Thr	Asp	Ile 55	Gly	Thr	Ser	Val	Gly 60	Thr	Gly	Gly	Lys
				3	<b>33</b> -	///		~1	T10	mb	T 011		77-7	7~~	C1.,	A cro
2194 2195	Ser 65	Asn	Asp	Asp	Ala	70	vai	GIU	116	1111	75	ASP	vai	Arg	GIU	80
2196	Ser	Val	Ala	Val	His	Ser	Val	Lvs	Thr	Ala	Glv	Gly	Asp	Asp	Val	Glu
2197					85			•		90	•	-	-	-	95	
2198	7.00	Dro	Glu	T.011		T.011	T.e.11	Δla	Larg		T.e.11	G111	Lvs	Lvs	Ser	Thr
	ASP	FIO	GIU	100	AIG	neu	шси	n_u	105	013			_,_	110		
2199	_	~ 7	_			**- 7	<b>3</b>	3		<b></b>	a	7	<b>T</b> 7.0		C1-	77-7
2200	Leu	GIY		ser	Leu	vai	Arg		Ala	ser	ser	Arg			GIII	vai
2201			115					120				_	125			
2202	Ser	Gln	Glu	Leu	Arg	Arg	Leu	Ala	Ser	Leu	Asn		Arg	Pro	IIe	Pro
2203		130					135					140				
2204	Thr	Gly	Arg	Phe	Asp	Arg	Asn	Lys	Ser	Ala	Ala	Ala	His	Ala	Leu	Lys
2205	145					150					155					160
2206	Glv	Leu	Lvs	Phe	Ile	Ser	Lys	Thr	Asp	Gly	Gly	Ala	Gly	Trp	Ala	Ala
2207	2		-2		165		•		-	170	_		_	_	175	
2208	17 = 1	Glu	Taye	Ara		Asp	Glu	Tle	Thr	Ala	Ser	Thr	Thr	Glv	Leu	Leu
2209			2,5	180		₽			185					190		
2210	Dwo	7~~	71-		Dhe	Glaz	Glu	Cvc		Glaz	Met	Agn	Lvc		Ser	Lvs
	PIO	Arg		Буб	FILE	Gry	Giu	200	110	GIŞ	Mec	T.DII	205	014	501	2,2
. 2211		-1	195		<b>a</b> 1	<b>-</b>	m		77-	T	71-	7		7-~	7 cm	Tlo
2212	GIu		Ala	vaı	Glu	Leu		Asp	Ala	Leu	Ala		Arg	Arg	ASII	116
2213		210			_		215			_	_	220	_,	_		<b>63</b> -
2214	Thr	Thr	Asp	Ser	Ile		Lys	Ala	Gln	Leu		GIu	Pne	Trp	Asp	
2215						230					235			_		240
2216	Val	Ala	Asp	Gln	Ser	Phe	Asp	Ser	Arg	Leu	Gln	Thr	Phe	Phe		Met
2217					245					250					255	
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2219				260					265					270		
2220	Ile	Ile	Gly	Leu	Ser	Ala	Ser	Ala	Asn	Arg	Leu	Ser	Thr	Ile	Gln	Lys
2221			275					280					285			
2222		Ala	Asp	Glu	Tvr	Ala	Ala	Met	Ile	Met	Glu	Glu	Leu	Asp	Pro	Asn
2223		290			•		295					300		_		
2224				Tvr	Tle	Met		Glu	Àsn	Leu	Glu	Met	Leu	Leu	Leu	Gln
2225			017	-1-		310					315					320
2226			Acn	GI n	Ser		Gl n	Ara	Glv	Glv		Ser	Ara	Asn	Leu	Ser
2227		110	TOIL	0111	325				U-1	330			5		335	
2228		M-+	T	C			T 011	Trea	ui c			G1.,	7 20	Acn	-	Tle
		Met	теп			шур	neu	шуз			GIII	Giu	m 9	350		-1-0
2229		_	_	340		<b>~</b>	<b>51</b>		345		T	T	3			C1-
		Arg			гĀг	ser	Pne			Pne	. теп	ьeu			пр	Gln
2231			355					360					365		_	_,
2232	Arg	Val	Trp	Val	Leu	Leu	Leu	Trp	Ile	Gly	Ile	Met	Ala	GLY	Leu	Phe
2233		370					375					380				
2234	Thr	Trp	Lys	Tyr	·Ile	Gln	Tyr	Lys	Glu	Lys	Ala	Ala	Tyr	Lys	Val	Met
2235			_	-		390					395					400
			Cvs	Val	Cvs	Phe	Ala	Lys	Gly	Ala	Ala	Glu	Thr	Leu	Lys	Leu
2237					405			•	•	410		·			415	
		Met	Ala	Ile			Phe	Pro	Val			Asn	Thr	Ile	Thr	Trp
2239				420					425		3			430		-
		2	, A ~~			· Δ~~	T.e.1	GI v			. Val	Pro	Pho			Asn
2240	חבו	, wr	, ASI	гъха	. 1111	Arg	ή <del>ς</del> υ	. Эту	тта			-10		بر ت	-101	

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005 TIME: 15:31:42

Input Set : A:\Sequence Listing.txt
Output Set: N:\CRF4\02022005\J522106.raw

435 440 445 2242 Leu Asn Phe His Lys Val Ile Ala Val Ala Ile Ala Leu Gly Val Gly 2244 Ile His Gly Leu Ser His Leu Thr Cys Asp Phe Pro Arg Leu Leu Asn 470 475 2246 Ala Ser Glu Glu Glu Tyr Glu Pro Met Lys Tyr Tyr Phe Gly Asp Gln 485 490 2247 2248 Pro Glu Ser Tyr Trp Trp Phe Ile Lys Gly Val Glu Gly Val Thr Gly 500 505 2250 Ile Ile Met Val Val Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Pro 520 2251 2252 Trp Phe Arg Arg Asn Arg Val Ser Leu Pro Lys Pro Phe His Lys Leu 2253 530 535 E--> 2254 Thr Gly Xaa Asn Ala Phe Trp Tyr Ser His His Leu Phe Val Ile Val 2255 545 550 555 2256 Tyr Thr Leu Phe Ile Val His Gly Glu Lys Leu Tyr Ile Thr Lys Asp 570 575 565 2258 Trp Tyr Lys Arg Thr Asp Met Asp Val Leu Leu Thr Ile Pro Ile Ile 585 580 . 2260 Leu Tyr Ala Ser Glu Arg Leu Ile Arg Ala Phe Arg Ser Ser Ile Lys 2261 595 600 2262 Ala Val Lys Ile Leu Lys Val Ala Val Tyr Pro Gly Asn Val Leu Ala 615 620 2264 Leu His Met Ser Lys Pro Gln Gly Tyr Lys Tyr Lys Ser Gly Gln Tyr 630 635 2266 Met Phe Val Asn Cys Ala Ala Val Ser Pro Phe Glu Trp His Pro Phe 650 2268 Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His Ile Arg 665 2270 Thr Leu Gly Asp Trp Thr Arg Gln Leu Lys Thr Val Phe Ser Glu Val 680 675 2272 Cys Gln Pro Pro Pro Asn Gly Lys Ser Gly Leu Leu Arg Ala Asp Tyr 695 690 2274 Leu Gln Gly Glu Asn Asn Pro Asn Phe Pro Arg Val Leu Ile Asp Gly 710 715 2276 Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr Glu Val Val Leu 730 725 2278 Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile Ser Ile Val Lys 740 745 2280 Asp Ile Val Asn Asn Met Lys Ala Met Asp Glu Glu Glu Asn Ser Leu 755 760 2282 Glu Asp Gly His Asn Asn Met Ala Pro Asn Ser Ser Pro Asn Ile 2283 770 - 775 780 2284 Ala Lys Asn Lys Gly Asn Lys Ser Gly Ser Ala Ser Gly Gly Asn Asn 790 795 2286 Phe Asn Thr Arg Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly 805 810 2288 Ser Phe Asp Trp Phe Lys Gly Ile Met Asn Glu Ala Ala Glu Met Asp 820

PIS See erronation RAW SEQUENCE LISTING

DATE: 02/02/2005

PATENT APPLICATION: US/10/522,106

TIME: 15:31:42

2290 2291	His	Lys	Gly 835	Val	Ile	Glu	Met	His 840	Asn	Tyr	Cys	Thr	Ser 845	Val	Tyr	Glu
2292 2293	Glu	Gly 850	Asp	Ala	Arg	Ser	Ala 855	Leu	Ile	Thr	Met	Leu 860	Gln	Ser	Leu	His
2294 2295		Ala	Lys	Asn	Gly	Val 870	Asp	Ile	Val	Ser	Gly 875	Thr	Arg	Val	Lys	Ser 880
2296 2297	His	Phe	Ala	Lys	Pro 885	Asn	Trp	Arg	Asn	Val 890	Tyr	Lys	Arg	Ile	Ala 895	Leu
2298 2299	Asn	His	Pro	Glu 900	Ala	Lys	Val	Gly	Val 905	Phe	Tyr	Cys	Gly	Ala 910	Pro	Ala
2300 2301	Leu	Thr	Lys 915	Glu	Leu	Arg	Gln	His 920	Ala	Leu	Asp	Phe	Ser 925	His	Lys	Thr
2302 2303	Ser	Thr 930	Lys	Phe	Asp	Phe	His 935	Lys	Glu	Asn	Phe					

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/522,106

DATE: 02/02/2005 TIME: 15:31:43

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\02022005\J522106.raw,

Use of n's or Xaa's (NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which

residue n or Xaa represents.

Seq#:1; Xaa Pos. 55

Seq#:2; Xaa Pos. 55

Seq#:15; Xaa Pos. 547 Seq#:16; Xaa Pos. 547

Seq#:15; N Pos. 1952

# VERIFICATION SUMMARY DATE: 02/02/2005 PATENT APPLICATION: US/10/522,106 TIME: 15:31:43

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:15 M:283 W: Missing Blank Line separator, <210> field identifier
L:19 M:283 W: Missing Blank Line separator, <220> field identifier
L:23 M:283 W: Missing Blank Line separator, <400> field identifier
L:34 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:193
L:49 M:283 W: Missing Blank Line separator, <400> field identifier
L:56 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:69 M:283 W: Missing Blank Line separator, <220> field identifier
L:73 M:283 W: Missing Blank Line separator, <400> field identifier
L:255 M:283 W: Missing Blank Line separator, <400> field identifier
L:379 M:283 W: Missing Blank Line separator, <220> field identifier
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L:570 M:283 W: Missing Blank Line separator, <400> field identifier
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L:904 M:283 W: Missing Blank Line separator, <400> field identifier
L:1032 M:283 W: Missing Blank Line separator, <220> field identifier
L:1036 M:283 W: Missing Blank Line separator, <400> field identifier
L:1234 M:283 W: Missing Blank Line separator, <400> field identifier
L:1364 M:283 W: Missing Blank Line separator, <220> field identifier
L:1368 M:283 W: Missing Blank Line separator, <400> field identifier
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L:1680 M:283 W: Missing Blank Line separator, <220> field identifier
L:1684 M:283 W: Missing Blank Line separator, <400> field identifier
L:1868 M:283 W: Missing Blank Line separator, <400> field identifier
L:1990 M:283 W: Missing Blank Line separator, <220> field identifier
L:1994 M:283 W: Missing Blank Line separator, <400> field identifier
L:2102 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:1935
M:341 Repeated in SeqNo=15
L:2185 M:283 W: Missing Blank Line separator, <400> field identifier
L:2254 M:340 E; (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:2309 M:283 W: Missing Blank Line separator, <220> field identifier
L:2313 M:283 W: Missing Blank Line separator, <400> field identifier
L:2477 M:283 W: Missing Blank Line separator, <400> field identifier
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L:3193 M:283 W: Missing Blank Line separator, <400> field identifier
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#### SEQUENCE LISTING

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       Huckelhoven, Ralph
       Trujillo, Marco
<120> Method for Obtaining the pathogenic resistance in plants
<130> 12810-00067-US
<140> US 10/522,106
<141> 2005-01-24
<160> 24
<170> PatentIn version 3.3
<210> 1
<211> 337
<212> DNA
<213> Hordeum vulgare
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<221> CDS
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<223> coding for NADPH oxidase (fragment)
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att gag atg cac aac tat ctc aca agt gtt tat gag gaa ggg gat gct
Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
                                 25
cgg tca gca ctc atc aca atg ctg caa gct ctc aac cat gcc aag aat
                                                                   145
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn
         35
                             40
                                                  45
ggt gtc gat gta gtg tct ggm act cga gtc cgg aca cat ttt gca aga
                                                                   193
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
                         55
                                              60
cca aat ttt aag agg gtg ctg tct aag gta gcc gcc aaa cat cct tat
                                                                   241
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
                     70
                                         75
gcc aag ata gga gtg ttc tat tgc gga gct cca gtt ctg gcg cag gaa
                                                                   289
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
                 85 -
                                     90
cta age aac ctt tgc cat gag ttc aat ggc aaa tgc acg aca aaa ttc
                                                                   337
Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe
                                105
<210> 2
<211> 112
<212> PRT
<213> Hordeum vulgare
<220>
<221> misc_feature
<222>
      (55)..(55)
<223> The 'Xaa' at location 55 stands for Gly.
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Phe Lys Gly Ile Met Asn Glu Ile Ala Glu Leu Asp Gln Arg Asn Ile

```
10
Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala
                                25
Arg Ser Ala Leu Ile Thr Met Leu Gln Ala Leu Asn His Ala Lys Asn
                            40
Gly Val Asp Val Val Ser Xaa Thr Arg Val Arg Thr His Phe Ala Arg
                        55
Pro Asn Phe Lys Arg Val Leu Ser Lys Val Ala Ala Lys His Pro Tyr
                    70
Ala Lys Ile Gly Val Phe Tyr Cys Gly Ala Pro Val Leu Ala Gln Glu
                85
                                    90
Leu Ser Asn Leu Cys His Glu Phe Asn Gly Lys Cys Thr Thr Lys Phe
                               105
<210> 3
<211> 2832
<212> DNA
<213> Oryza sativa
<220>
<221> CDS
<222> (1)..(2829)
<223> coding for NADPH oxidase
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Met Arg Gly Gly Ala Ser Ser Gly Pro Gln Arg Trp Gly Ser Ala Gly
acg aca ccg cgg tcg ctg agc acg ggc tcg tcg ccg cgc ggg tcc gac
Thr Thr Pro Arg Ser Leu Ser Thr Gly Ser Ser Pro Arg Gly Ser Asp
            20
                                25
                                                                144
gac egg age tee gac gac ggg gag gag etg gtc gag gtc acg etc gac
Asp Arg Ser Ser Asp Asp Gly Glu Glu Leu Val Glu Val Thr Leu Asp
        35
                            40
                                                                192
ctg cag gac gac acc att gtg ctt cgg agc gtc gag ccc gcg gcg
Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala
                        55
240
Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ala Ser Ala Arg
ggg gag ctc acg ggt ggc ccg tcg tcg tcg tcg tcg cgg tcg agg tcg
                                                                288
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Arg Ser Arg Ser
ccg tcg atc cgg agg agc tcg tcg cac cgg ctg ctg cag ttc tcg cag
                                                                336
Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln
                               105
gag etc aag geg gag gec atg gee egg geg eag tte teg eag gae
                                                                384
Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp
       115
                           120
                                                                432
ctg acc aag cgg ttc ggc cgc agc cac agc cgc agc gaa gcg cag gcg
Leu Thr Lys Arg Phe Gly Arg Ser His Ser Arg Ser Glu Ala Gln Ala
                       135
                                           140
ceg teg gge ete gag tee geg ete gee ege gee geg egg egg eag
                                                                480
Pro Ser Gly Leu Glu Ser Ala Leu Ala Ala Arg Ala Arg Arg Gln
                   150
                                       155
cgc gcg cag ctc gac cgc aca cgc tcc ggc gcc cac aag gcg ctc cgc
                                                                528
Arg Ala Gln Leu Asp Arg Thr Arg Ser Gly Ala His Lys Ala Leu Arg
                                   170
               165
gge etc ege tte ate age age aae aag gee aae aae gee tgg atg gag
                                                                576
Gly Leu Arg Phe Ile Ser Ser Asn Lys Ala Asn Asn Ala Trp Met Glu
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		gcc Ala 195														624
Ser	Asp 210	ttc Phe	Āla	Glu	Cys	Ile 215	Gly	Met	Thr	Glu	Ser 220	Lys	Glu	Phe	Ala	672
		ctg Leu		-	_	-	-		-	_	_	_	_		-	720
_		aac Asn	_	_	_		_				_	_			-	768
		ttc Phe														816
		gac Asp 275														864
		gcg Ala														912
		gcc Ala														960
		gag Glu														1008
		aac Asn														1056
_		ctt Leu 355	_				_	_	_			-			_	1104
		tta Leu	_					-				_				1152
		ttg Leu														1200
_	_	tat Tyr	_		_		-		-		_			_	-	1248
		gca Ala														1296
		ctg Leu 435		_	-	_						_	_	_		1344
		gca Ala														1392
		gca Ala														1440
		gta Val		-									_		_	1488
		cct Pro														1536
aca	ttg	gtc	aaa	gga	gtg	gag	ggc	atc	act	ggg	gta	atc	atg	gtt	gta	1584

	Leu	515					520					525				,
	atg Met 530															1632
	gtt Val															1680
ttt	tgg Trp			His	cat				Ile	gtg				Leu	att	1728
	cat His		Glu					Ile					Arg			1776
	tgg Trp															1824
	cta Leu															1872
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gca	gtg	tct	ccc	645 ttt	gaa	tgg	cat	ccc	650 ttc	tca	att	act	tca	655 gca	cct	2016
	Val gat		660			_		665					670			2064
Gly	Āsp	Asp 675	Tyr	Leu	Ser	Ile	His 680	Val	Arg	Gln	Leu	Gly 685	Asp	Trp	Thr	2112
Arg	Glu 690	Leu	Lys	Arg	Val	Phe 695	Ala	Ala	Ala	Cys	Glu 700	Pro	Pro	Ala	Gly	
Gly 705	aaa Lys	Ser	Gly	Leu	Leu 710	Arg	Ala	Asp	Glu	Thr 715	Thr	Lys	Lys	Ile	Leu 720	2160
	aag Lys															2208
_	aag Lys			gtt					-							2256
	ttt Phe		_				_		_						_	2304
	gaa Glu 770															2352
	aag Lys			-	_	_				_	_				_	2400
cca	aag Lys															2448
_	gag Glu			tct					aaa		_	_		gaa		2496
	gac Asp		gat					att					tac			2544

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840
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Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu
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                                            860
                                                                   2640
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Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr
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Lys Val Arg Thr His Phe Ala Arg Pro Asn Trp Arg Lys Val Leu Ser
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Lys Ile Ser Ser Lys His Pro Tyr Ala Lys Ile Gly Val Phe Tyr Cys
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Leu Gln Asp Asp Asp Thr Ile Val Leu Arg Ser Val Glu Pro Ala Ala
Ala Ala Ala Gly Val Gly Ala Gly Ala Gly Ala Ala Ser Ala Arg
Gly Glu Leu Thr Gly Gly Pro Ser Ser Ser Ser Arg Ser Arg Ser
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Pro Ser Ile Arg Arg Ser Ser Ser His Arg Leu Leu Gln Phe Ser Gln
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Glu Leu Lys Ala Glu Ala Met Ala Arg Ala Arg Gln Phe Ser Gln Asp
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Val Gln Ala Asn Phe Asp Arg Leu Ala Arg Asp Gly Tyr Leu Ser Arg
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Leu Glu Leu Phe Asp Thr Leu Ser Arg Arg Gln Met Lys Val Asp
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Thr Ile Asn Lys Asp Glu Leu Arg Glu Ile Trp Gln Gln Ile Thr Asp
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Asn Ala Asp Gly Arg Ile Thr Glu Ala Glu Val Lys Glu Ile Ile Met
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Gly Tyr Asn Ser Gly Phe Ala Ser Glu Glu Phe Val Glu Val Thr Leu
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	aca Thr															1200
	ctc Leu															1248
	tat Tyr								Phe							1296
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	gcg Ala															400
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	gct Ala															496
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	gcg Ala															592
	tcg Ser															640
	cgg Arg 185															688
	agc Ser															736
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	cga Arg								Leu							2032
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				gac Asp												2320
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				gaa Glu 940												2944
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ttg	acct	tct	tgat	aaaga	aa a	cacta	atgaa	a aa	tggc	aagc	atga	aaag	gac a	agac	aatcat ggagta	3410

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Lys	Phe	Tyr	Leu 420	405 Tyr	Lys	Gln	Lys	Ser 425	410 Ala	Phe	Gln	Va·l	Met 430	415 Gly	Tyr
Суѕ	Leu	Leu 435	Thr	Ala	Lys	Gly	Ala 440		Glu	Thr	Leu	Lys 445		Asn	Met
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Val Phe Tyr Cys Gly Ala Pro Ile Leu Ala Lys Glu Leu Ser Lys Leu
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Arg Trp Thr Ser Asp Thr Val Ser Ser Gly Lys Asp Leu Ser Gly Glu
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Ser Ser Pro Gly Thr Asp Ser Gly Asn Ile Ser Gly Phe Ala Ser Glu
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Glu Phe Val Glu Val Ile Leu Asp Leu Gln Asp Asp Asp Thr Ile Ile
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cct gct tcc gga gtc ggt att ggt gga gca tcg att gaa act ccg gcg
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Pro Ala Ser Gly Val Gly Ile Gly Gly Ala Ser Ile Glu Thr Pro Ala
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Ser Val Thr Ser Thr Ser Glu Thr Arg Ser Pro Met Met Arg Arg Ser
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Thr Ser Asn Lys Phe Arg Gln Phe Ser Gln Glu Leu Lys Ala Glu Ala
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Val Ala Lys Ala Lys His Phe Ser Gln Glu Leu Lys Ala Glu Leu Arg
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                                130
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Arg Phe Ser Trp Ser His Gly His Ala Ser Arg Ala Phe Ser Pro Ala
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                                                 150
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	Ala	220	_				225					230				0.00
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	Thr	300					305					310				1100
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	Ala			350					355					360		1076
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	Asp															
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	Leu 395					400	_				405					4 4 0 0
	atg															1420
Arg 410	Met	Ser	Thr	ьys	415	var	Tyr	ser	ьeu	420	GIU	ASII	пр	гуу	425	
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Trp	Lys	Phe	Tyr 445	Gln	Tyr	Lys	Gln	Lys 450	Ser	Ala	Phe	Gln	Val 455	Met	Gly	
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Tyr	Cys		Leu	Thr	Ala	Lys		Ala	Ala	Glu	Thr		Lys	Phe	Asn	
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	tct															1660
Arg 490	Ser	Tur	гàг	ьeu	Ser 495	Cys	rue	vaı	PTO	500	Asp	Asp	ASN	тте	505	
4 J U					<u> </u>					500					555	

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	acg Thr															1804
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	Gly															2140
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	cag Gln															2284
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	cca Pro															2428
	aca Thr															2476
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                                                 870
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                             40
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Ser Gln Glu Leu Lys Ala Glu Leu Arg Arg Phe Ser Trp Ser His Gly
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His Ala Ser Arg Ala Phe Ser Pro Ala Ser Phe Phe Gln Asn Ala Val
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	ac ac				atg					att							290
	aa cg /s Ar			tca													338
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tcg Ser	atc Ile	tcg Ser	gat Asp	ttc Phe 785	agt Ser	aga Arg	tca Ser	tca Ser	gaa Glu 790	tac Tyr	agc Ser	aca Thr	gga Gly	agc Ser 795	aac Asn	2402
							aga Arg									2450
ttc Phe	tac Tyr	tgg Trp 815	gtc Val	aca Thr	aga Arg	gaa Glu	caa Gln 820	ggc	tct Ser	ttt Phe	gat Asp	tgg Trp 825	ttc Phe	aaa Lys	ggt Gly	2498
							ctt Leu									2546
							tat Tyr									2594
			_	-		_	ctt Leu									2642
att Ile	gtc Val	tct Ser	ggc Gly 880	act Thr	agg Arg	gtc Val	aga Arg	aca Thr 885	cac His	ttt Phe	gca Ala	aga Arg	cct Pro 890	aat Asn	tgg Trp	2690
_	_	_					agt Ser 900								_	2738
							ccg Pro									2786
							aaa Lys									2834
				taa	aaga	caa	gaag	gaag	aa g	ccaa	aagc	c ct	ctag	attc		2886
aag gag cat ttc taaaagacaa gaaggaagaa gccaaaagcc ctctagattc Lys Glu His Phe tttaatatct caaatttagc cacttatagt ataaaggcaa tctcttcact atttaattca aagtgattaa acgttaacac actgtcaaaa gtgagtgtgt taacgtttag ctccacacgt tctaggttta tatacaccga ggcatacgtg taaatatacg agacagaaga aattcaaggg ggtttgatag aagc												3006				

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Ile Leu His Ile Gly Asp His Leu Ala Cys Asp Phe Pro Arg Ile Val Arg Ala Thr Glu Tyr Asp Tyr Asn Arg Tyr Leu Phe His Tyr Phe Gln Thr Lys Gln Pro Thr Tyr Phe Asp Leu Val Lys Gly Pro Glu Gly Ile Thr Gly Ile Leu Met Val Ile Leu Met Ile Ile Ser Phe Thr Leu Ala Thr Arg Trp Phe Arg Arg Asn Leu Val Lys Leu Pro Lys Pro Phe Asp Arg Leu Thr Gly Phe Asn Ala Phe Trp Tyr Ser His His Leu Phe Val Ile Val Tyr Ile Leu Leu Ile Leu His Gly Ile Phe Leu Tyr Phe Ala Lys Pro Trp Tyr Val Arg Thr Thr Trp Met Tyr Leu Ala Val Pro Val Leu Leu Tyr Gly Gly Glu Arg Thr Leu Arg Tyr Phe Arg Ser Gly Ser Tyr Ser Val Arg Leu Leu Lys Val Ala Ile Tyr Pro Gly Asn Val Leu Thr Leu Gln Met Ser Lys Pro Thr Gln Phe Arg Tyr Lys Ser Gly Gln Tyr Met Phe Val Gln Cys Pro Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Glu Asp Asp Tyr Ile Ser Ile His Ile Arg Gln Leu Gly Asp Trp Thr Gln Glu Leu Lys Arg Val Phe Ser Glu Val Cys Glu Pro Pro Val Gly Gly Lys Ser Gly Leu Leu Arg Ala Asp Glu Thr Thr Lys Lys Ser Leu Pro Lys Leu Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Arg Lys Tyr Asp Val Leu Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Val Lys Met Glu Glu His Ala Asp Ser Ile Ser Asp Phe Ser Arg Ser Ser Glu Tyr Ser Thr Gly Ser Asn Gly Asp Thr Pro Arg Arg Lys Arg Ile Leu Lys Thr Thr Asn Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Asp Trp Phe Lys Gly Val Met Asn Glu Val Ala Glu Leu Asp Gln Arg Gly Val Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Val Gln Ala Leu Asn His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg Val Arg Thr His Phe Ala Arg Pro Asn Trp Lys Lys Val Leu Thr Lys Leu Ser Ser Lys His Cys Asn Ala Arg Thr Gly Val Phe Tyr Cys Gly Val Pro Val Leu Gly Lys Glu Leu Ser Lys Leu Cys Asn Thr Phe Asn Gln Lys Gly Ser Thr Lys Phe Glu Phe His Lys Glu His Phe 

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tctcgaattc g atg aaa atg aga cga ggc aat tca agt aac gac cat gaa
             Met Lys Met Arg Arg Gly Asn Ser Ser Asn Asp His Glu
ctt ggg att cta cga gga gct aac tcg gac acc aac tcg gac acg gag
                                                                   218
Leu Gly Ile Leu Arg Gly Ala Asn Ser Asp Thr Asn Ser Asp Thr Glu
                         20
                                             25
                                                                   266
age ate get age gae egt ggt gee tit age ggt eeg ett gge egg eet
Ser Ile Ala Ser Asp Arg Gly Ala Phe Ser Gly Pro Leu Gly Arg Pro
                     35
aaa cgt gcg tcc aag aaa aac gca aga ttc gcc gac gat ctt ccc aag
                                                                   314
Lys Arg Ala Ser Lys Lys Asn Ala Arg Phe Ala Asp Asp Leu Pro Lys
                                     55
                 50
aga agc aat agt gtt gct ggc ggc cgt ggt gat gac gat gag tac gtg
                                                                   362
Arg Ser Asn Ser Val Ala Gly Gly Arg Gly Asp Asp Asp Glu Tyr Val
                                                                   410
gag atc acg cta gac atc agg gac gac tcg gtg gcc gtc cat agt gtc
Glu Ile Thr Leu Asp Ile Arg Asp Asp Ser Val Ala Val His Ser Val
                             85
caa caa gca gct gga ggt gga ggc cac ctg gag gac ccg gag cta gcc
                                                                   458
Gln Gln Ala Ala Gly Gly Gly His Leu Glu Asp Pro Glu Leu Ala
                        100
                                                                   506
ctt ctt acg aag aag act ctc gag agc agc ctc aac aac acc acc tcc
Leu Leu Thr Lys Lys Thr Leu Glu Ser Ser Leu Asn Asn Thr Thr Ser
                                        120
                    115
tta tct ttc ttc cga agc acc tcc tca cgc atc aag aac gcc tcc cgc
Leu Ser Phe Phe Arg Ser Thr Ser Ser Arg Ile Lys Asn Ala Ser Arg
                130
                                    135
gag ctc cgc cgc gtg ttc tct aga cgt ccc tcc ccg gcc gtg cgg cgg
                                                                   602
Glu Leu Arg Arg Val Phe Ser Arg Arg Pro Ser Pro Ala Val Arg Arg
                                150
                                                                   650
ttt gac ege aeg age tee geg gee ate eae gea ete aaa ggt ete aag
Phe Asp Arg Thr Ser Ser Ala Ala Ile His Ala Leu Lys Gly Leu Lys
                            165
                                                 170
                                                                   698
ttc att gcc acc aag acg gcc gca tgg ccg gcc gtc gac caa cgt ttc
Phe Ile Ala Thr Lys Thr Ala Ala Trp Pro Ala Val Asp Gln Arg Phe
    175
                        180
gat aaa ctc tcc gct gat tcc aac ggc ctc tta ctc tct gcc aag ttt
                                                                   746
Asp Lys Leu Ser Ala Asp Ser Asn Gly Leu Leu Ser Ala Lys Phe
                    195
                                         200
tgg gaa tgc tta gga atg aat aag gaa tct aaa gac ttc gct gac cag
Trp Glu Cys Leu Gly Met Asn Lys Glu Ser Lys Asp Phe Ala Asp Gln
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ctc ttt aga gca tta gct cgc cgg aat aac gtc tcc ggc gat gca atc
Leu Phe Arg Ala Leu Ala Arg Arg Asn Asn Val Ser Gly Asp Ala Ile
                                230
aca aag gaa cag ctt agg ata ttc tgg gaa cag atc tca gac gaa agc
Thr Lys Glu Gln Leu Arg Ile Phe Trp Glu Gln Ile Ser Asp Glu Ser
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ttt qat qcc aaa ctc caa gtc ttt ttt gac atg gtg gac aaa gat gaa
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Phe Asp Ala Lys Leu Gln Val Phe Phe Asp Met Val Asp Lys Asp Glu

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		Arg														
270					275					280					285	1004
-		gca		_						_		_		-		1034
Ald	ser	Ala	ASII	290	Leu	Ser	ASII	TTE	295	гу	GIII	Ата	гуу	300	ıyı	•
aca	qca	ctg	ata		gaa	gag	ttq	gac		gac	aat	gct	qqq		att	1082
		Leu														
			305					310					315			
		gaa														1130
Met	IIe	Glu	Asn	Leu	Glu	Met	ьеи 325	Leu	Leu	GIn	Ala	330	Asn	Gin	Ser	
ata	caa	320 atg	ααa	gac	agc	agg		ctt	aαt	саσ	atα		agt	cag	aaq	1178
		Met														
	335		_	_		340					345					
		ccg														1226
	Arg	Pro	Ala	Lys		Ser	Asn	Pro	Leu		Arg	Trp	Ser	Glu		
350	222	tat	++~	a+a	355 ctt	aat	aat	taa	cad	360	tta	taa	atc	ato	365 at o	1274
		Tyr														12,1
	-1-	-1-		370					375			1		380		
		ctt														1322
Leu	Trp	Leu	-	Ile	Cys	Gly	Gly		Phe	Thr	Tyr	Lys		Ile	Gln	
+	224	aac	385	aat	aaa`	+ - +	aat	390	2+4	aat	+ > +	+~+	395	+ ~+	ata	1370
		Asn														1370
-1-	_,_	400	2,0			-1-	405			0-1	- 1 -	410		-1-		
gcc	aaa	gga	ggc	gcc	gag	act	ctc	aaa	ttc	aac	atg	gct	ctc	ata	ttg	1418
Ala	_	Gly	Gly	Ala	Glu		Leu	Lys	Phe	Asn		Ala	Leu	Ile	Leu	
	415					420			<b>.</b>		425					1466
_		gtt Val	_	_												1466
430	110	VUI	Cys	1119	435	1111	110	****	115	440	1119	11011	,		445	
ctt	ggt	act	gtc	gtt	cct	ttt	gat	gat	agt	ctt	aac	ttc	cac	aag	gtt	1514
Leu	Gly	Thr	Val		Pro	Phe	Asp	Asp		Leu	Asn	Phe	His		Val	
		agc		450	~+~	~+~	~~+	~++	455	a+ a	a = +	~~~	~~+	460	an+	1562
		Ser														1302
			465				1	470					475			
		tgt														1610
Leu	Thr	Cys	Asp	Phe	Pro	Arg		Ile	Ala	Ala	Asp		Asp	Thr	Tyr	
~~~	000	480 atg	<b>~</b> 2 2	222	+ = 0	+++	485	~a+	C22	cca	a c+	490	t a c	taa	taa	1658
		Met														1000
	495			-1-	-1-	500	1				505		- 1		1	
		aaa														1706
	Val	Lys	Gly	Val		Gly	Trp	Thr	Gly		Val	Met	Val	Val		
510	ac+	a+ a	~~~	+++	515	c+c	act	200	cct	520	++~	cas	cat	220	525	1754
_	_	ata Ile	_													1/54
				530					535			9		540	-1-	
		tta														1802
Leu	Asn	Leu		Asn	Phe	Leu	Lys		Leu	Thr	Gly	Phe		Ala	Phe	
+~~	t=~	acc	545	c=+	++~	++0	ato	550	α++	t a t	ac+	c++	555 ct c	att	atc	1850
		Thr			_				_		-				_	1000
	- <b></b> _	560					565			- 1 -		570				
		atc	_					_				_	_	_		1898
His	_	Ile	Lys	Leu	Tyr		Thr	Lys	Ile	Trp	_	Gln	Lys	Thr	Thr	
	575					580					585					

4.5. r

Trp	atg Met				Val					Tyr						1946
590	cgt	act	ttc	aga	595 t ca	agc	atc	aaa	cca	600 att	aaα	ato	atc	ааσ		1994
	Arg															2,7,1
gct	gtt	tac	ccc	ggg	aac	gtg	ttg	tct	cta	cac	atg	acg	aag	cca	caa	2042
	Val	_	625	_				630					635			
	ttc															2090
_	Phe	640	_	_			645					650				0120
	tct															2138
	Ser 655					660					665					
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670	Asp	_			675					680					685	
	ctc															2234
_	Leu	_		690					695					700		
	agc															2282
_	Ser	_	705					710					715			
	aag															2330
	Lys	720					725					730				0070
aag	aaa	tac	gac	gtg	gta	ctc	ctc	gta	ggt	ctc	ggc	att	gga	gcc	acg	2378
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	atg															2426
750	Met				755	_	_			760					765	0.47.4
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_	Arg	_		770					775					780		2522
	ttt															2522
	Phe	_	785					790					795			
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_	Ser	800		_			805					810				
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_	Glu 815		-		-	820					825					
	gaa															2666
	Glu	Gly	Asp	Ala	Arg 835	Val	Ala	Leu	TTE	840	Met	Leu	GIN	Ser	ьеи 845	
830	G 2 G	act	224	330		ata	ca+	at t	at a		aat	202	cat	atc		2714
	cac His															2/14
ticc	cac	ttc	act		cct	aac	taa	aσa		atc	tac	aag	aaσ		act	2762
	His															
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	Gln	880		_	_		885					890				
	atg															2858
	Met 895					900					905				Lys	
aca	act	acc	aag	ttt	gac	ttc	cac	aaa	gag	aac	ttc	tag	atta	att		2904

Thr Thr Thr Lys Phe Asp Phe His Lys Glu Asn Phe 915 920 atatacgttg tagaaaaata aaacaagaaa caactataca aataaatatt tattttaaat 2964 tcttttcatt ttatgtaaaa ttatctgagt tatcttttt tgttaaaaaa aaaaaaaaa 3024 aaaaaaaaa a <210> 14 <211> 921 <212> PRT <213> Arabidopsis thaliana <400> 14 Met Lys Met Arg Arg Gly Asn Ser Ser Asn Asp His Glu Leu Gly Ile 10 15 Leu Arg Gly Ala Asn Ser Asp Thr Asn Ser Asp Thr Glu Ser Ile Ala 25 Ser Asp Arg Gly Ala Phe Ser Gly Pro Leu Gly Arg Pro Lys Arg Ala 40 Ser Lys Lys Asn Ala Arg Phe Ala Asp Asp Leu Pro Lys Arg Ser Asn Ser Val Ala Gly Gly Arg Gly Asp Asp Asp Glu Tyr Val Glu Ile Thr 70 Leu Asp Ile Arg Asp Asp Ser Val Ala Val His Ser Val Gln Gln Ala 90 85 Ala Gly Gly Gly His Leu Glu Asp Pro Glu Leu Ala Leu Leu Thr 100 105 Lys Lys Thr Leu Glu Ser Ser Leu Asn Asn Thr Thr Ser Leu Ser Phe 120 125 Phe Arg Ser Thr Ser Ser Arg Ile Lys Asn Ala Ser Arg Glu Leu Arg 135 140 Arg Val Phe Ser Arg Arg Pro Ser Pro Ala Val Arg Arg Phe Asp Arg 150 155 Thr Ser Ser Ala Ala Ile His Ala Leu Lys Gly Leu Lys Phe Ile Ala 170 165 Thr Lys Thr Ala Ala Trp Pro Ala Val Asp Gln Arg Phe Asp Lys Leu 185 180 Ser Ala Asp Ser Asn Gly Leu Leu Leu Ser Ala Lys Phe Trp Glu Cys 205 200 195 Leu Gly Met Asn Lys Glu Ser Lys Asp Phe Ala Asp Gln Leu Phe Arg 215 220 Ala Leu Ala Arg Arg Asn Asn Val Ser Gly Asp Ala Ile Thr Lys Glu 235 230 Gln Leu Arg Ile Phe Trp Glu Gln Ile Ser Asp Glu Ser Phe Asp Ala 250 Lys Leu Gln Val Phe Phe Asp Met Val Asp Lys Asp Glu Asp Gly Arg 265 270 Val Thr Glu Glu Val Ala Glu Ile Ile Ser Leu Ser Ala Ser Ala 280 Asn Lys Leu Ser Asn Ile Gln Lys Gln Ala Lys Glu Tyr Ala Ala Leu 295 300 Ile Met Glu Glu Leu Asp Pro Asp Asn Ala Gly Phe Ile Met Ile Glu 310 315 Asn Leu Glu Met Leu Leu Gln Ala Pro Asn Gln Ser Val Arg Met 325 . 330 Gly Asp Ser Arg Ile Leu Ser Gln Met Leu Ser Gln Lys Leu Arg Pro 340 345 Ala Lys Glu Ser Asn Pro Leu Leu Arg Trp Ser Glu Lys Ile Lys Tyr 360 365 355 Phe Ile Leu Asp Asn Trp Gln Arg Leu Trp Ile Met Met Leu Trp Leu

375

Gly Ile Cys Gly Gly Leu Phe Thr Tyr Lys Phe Ile Gln Tyr Lys Asn

385 Lvs	Ala	Ala	Tvr	Glv	390 Val	Met	Glv	Tvr	Cvs	395 Val	Cvs	Val	Ala	Lvs	400 Gly
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-	Ala		420					425					430		
_	Arg	435					440					445			
Val	Val 450	Pro	Phe	Asp	Asp	Ser 455	Leu	Asn	Phe	His	Lys 460	Val	Ile	Ala	Ser
Gly 465	Ile	Val	Val	Gly	Val 470	Leu	Leu	His	Ala	Gly 475	Ala	His	Leu	Thr	Cys 480
Asp	Phe	Pro	Arg	Leu 485	Ile	Ala	Ala	Asp	Glu 490	Asp	Thr	Tyr	Glu	Pro 495	Met
Glu	Lys	Tyr	Phe 500	Gļy	Asp	Gln	Pro	Thr 505	Ser	Tyr	Trp	Trp	Phe 510	Val	Lys
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Phe	Arg 610	Ser	Ser	Ile	Lys	Pro 615	Val	Lys	Met	Ile	Lys 620	Val	Ala	Val	Tyr
Pro 625	Gly	Asn	Val	Leu	Ser 630	Leu	His	Met	Thr	Lys 635	Pro	Gln	Gly	Phe	Lys 640
Tyr	Lys	Ser	Gly	Gln 645	Phe	Met	Leu	Val	Asn 650	Cys	Arg	Ala	Val	Ser 655	Pro
Phe	Glu	Trp	His 660	Pro	Phe	Ser	Ile	Thr 665	Ser	Ala	Pro	Gly	Asp 670	Asp	Tyr
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705	Leu				710					715					720
	Ile			725					730					735	
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Glu	Trp	Phe	Lys	Gly 805	Ile	Met	Asp	Glu	Ile 810	Ser	Glu	Leu	Asp	Glu 815	
Gly	Ile	Ile	Glu 820	Leu	His	Asn	Tyr	Cys 825	Thr	Ser	Val	Tyr	Glu 830	Glu	Gly
Asp	Ala	Arg 835	Val	Ala	Leu	Ile	Ala 840	Met	Leu	Gln	Ser	Leu 845		His	Ala
Lys	Asn 850	Gly	Val	Asp	Val	Val 855	Ser	Gly	Thr	Arg	Val 860	Lys	Ser	His	Phe
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Lys Phe Asp Phe His Lys Glu Asn Phe
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acatettttt tteaacetat ettetteat ttteaagaat tegggtteea taaatagtag 240
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              Met Gln Asn Ser Glu Asn His His Pro His His Gln His
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cac cat tog gac aca gag ata att gga aat gat aga gog tog tac agt
His His Ser Asp Thr Glu Ile Ile Gly Asn Asp Arg Ala Ser Tyr Ser
                         20
                                             25
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Gly Pro Leu Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala
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                                         40
                                                                   495
aga ttt aac att cet gaa tet ace gac ate gga ace agt gte gga ace
Arg Phe Asn Ile Pro Glu Ser Thr Asp Ile Gly Thr Ser Val Gly Thr
                                     55
ggc ggc aag tcc aat gat gat gcg tac gtt gaa atc act ctc gat gtc
                                                                   543
Gly Gly Lys Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val
             65
                                                                   591
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Arg Glu Asp Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp
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                                                                   639
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Asp Val Glu Asp Pro Glu Leu Ala Leu Leu Ala Lys Gly Leu Glu Lys
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                                            105
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aag too act tta gga tot toa ott gtt oga aat got tog tot aga att
Lys Ser Thr Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile
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                                        120
cgg caa gtg tca caa gag ctc agg cgt ttg gct tcc tta aat aaa cgc
                                                                   735
Arg Gln Val Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg
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Pro Ile Pro Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala Ala His
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gct ctt aaa ggt ctc aag ttt att agt aag acc gac ggc ggc gct ggt
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Ala Leu Lys Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly
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170

160

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Val 270	Arg	Glu	Ile	Ile	ggc Gly 275	Leu	Ser	Ala	Ser	Ala 280	Asn	Arg	Leu	Ser	Thr 285	1167
					gat Asp											1215
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					aat Asn											1311
					cta Leu											1359
					tgg Trp 355											1407
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					aat Asn 435											1647
					ttt Phe											1695
					gga Gly											1743
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His	Lys	Leu	Thr 545	Gly	Xaa	Asn	Ala	Phe 550	Trp	Tyr	tct Ser	His	His 555	Leu	Phe	1983
Val	Ile	Val 560	Tyr	Thr	Leu	Phe	Ile 565	Val	His	Gly	gaa Glu	Lys 570	Leu	Tyr	Ile	2031
Thr	Lys 575	Asp	Trp	Tyr	Lys	Arg 580	Thr	Asp	Met	Asp	gta Val 585	Leu	Leu	Thr	Ile	2079
cca Pro 590	atc Ile	ata Ile	ctc Leu	tat Tyr	gct Ala 595	agt Ser	gaa Glu	agg Arg	ttg Leu	att Ile 600	agg Arg	gca Ala	ttc Phe	agg Arg	tca Ser 605	2127
agc Ser	att Ile	aaa Lys	gct Ala	gtt Val 610	aag Lys	att Ile	ttg Leu	aag Lys	gtg Val 615	gca Ala	gta Val	tat Tyr	cca Pro	gga Gly 620	aat Asn	2175
gtg Val	ttg Leu	gca Ala	ctt Leu 625	cac His	atg Met	tca Ser	aaa Lys	cca Pro 630	cag Gln	ggc Gly	tac Tyr	aaa Lys	tac Tyr 635	aaa Lys	agt Ser	2223
Gly	caa Gln	tac Tyr 640	atg Met	ttt Phe	gtc Val	aac Asn	tgt Cys 645	gct Ala	gca Ala	gtt Val	tct Ser	cca Pro 650	ttt Phe	gag Glu	tgg Trp	2271
cat His	cca Pro 655	ttt Phe	tca Ser	att Ile	act Thr	tcg Ser 660	gcc Ala	cca Pro	gga Gly	gat Asp	gac Asp 665	tat Tyr	ctc Leu	agt Ser	gtc Val	2319
cat His 670	att Ile	cga Arg	act Thr	ctt Leu	ggt Gly 675	gat Asp	tgg Trp	acc Thr	agg Arg	caa Gln 680	ctt Leu	aaa Lys	act Thr	gtt Val	ttc Phe 685	2367
tcc Ser	gag Glu	gtt Val	tgc Cys	cag Gln 690	cca Pro	cca Pro	cct Pro	aat Asn	gga Gly 695	aaa Lys	agt Ser	gga Gly	ctc Leu	ctc Leu 700	aga Arg	2415
gct Ala	gac Asp	tac Tyr	ttg Leu 705	caa Gln	gga Gly	gag Glu	aat Asn	aat Asn 710	cct Pro	aat Asn	ttc Phe	cca Pro	agg Arg 715	gtg Val	tta Leu	2463
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Pro	Asn	Ile	Ala 785	Lys	Asn	Lys	Gly	Asn 790	Lys	Ser	ggt Gly	Ser	Ala 795	Ser	Gly	2703
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gaa Glu	caa Gln	ggt	tca	ttt Phe	gat Asp	tgg Trp	ttc Phe	aaa Lys	ggt Gly	ata Ile	atg Met	aat Asn	gaa Glu	gct Ala	gct Ala	2799

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gtt tat gaa gaa ggt gat gct cgt tct gct ctt att act atg ctt cag
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Val Tyr Glu Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln
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Ser Leu His His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg
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                                                 890
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Ile Ala Leu Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly
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Ala Pro Ala Leu Thr Lys Glu Leu Arg Gln His Ala Leu Asp Phe Ser
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                                                                   3129
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His Lys Thr Ser Thr Lys Phe Asp Phe His Lys Glu Asn Phe
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                                     935
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Ser Gly Pro Leu Asn Lys Arg Gly Gly Lys Lys Ser Ala Arg Phe Asn
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Ile Pro Glu Ser Thr Àsp Ile Gly Thr Ser Val Gly Thr Gly Gly Lys
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Ser Asn Asp Asp Ala Tyr Val Glu Ile Thr Leu Asp Val Arg Glu Asp
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                     70
Ser Val Ala Val His Ser Val Lys Thr Ala Gly Gly Asp Asp Val Glu
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                 85
Asp Pro Glu Leu Ala Leu Leu Ala Lys Gly Leu Glu Lys Lys Ser Thr
                                 105
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Leu Gly Ser Ser Leu Val Arg Asn Ala Ser Ser Arg Ile Arg Gln Val
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                                                 125
Ser Gln Glu Leu Arg Arg Leu Ala Ser Leu Asn Lys Arg Pro Ile Pro
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                         135
Thr Gly Arg Phe Asp Arg Asn Lys Ser Ala Ala Ala His Ala Leu Lys
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                                         155
Gly Leu Lys Phe Ile Ser Lys Thr Asp Gly Gly Ala Gly Trp Ala Ala
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Val Glu Lys Arg Phe Asp Glu Ile Thr Ala Ser Thr Thr Gly Leu Leu
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Pro Arg Ala Lys Phe Gly Glu Cys Ile Gly Met Asn Lys Glu Ser Lys Glu Phe Ala Val Glu Leu Tyr Asp Ala Leu Ala Arg Arg Arg Asn Ile Thr Thr Asp Ser Ile Asn Lys Ala Gln Leu Lys Glu Phe Trp Asp Gln Val Ala Asp Gln Ser Phe Asp Ser Arg Leu Gln Thr Phe Phe Asp Met Val Asp Lys Asp Ala Asp Gly Arg Ile Thr Glu Glu Glu Val Arg Glu Ile Ile Gly Leu Ser Ala Ser Ala Asn Arg Leu Ser Thr Ile Gln Lys Gln Ala Asp Glu Tyr Ala Ala Met Ile Met Glu Glu Leu Asp Pro Asn Asn Leu Gly Tyr Ile Met Ile Glu Asn Leu Glu Met Leu Leu Gln Ala Pro Asn Gln Ser Val Gln Arg Gly Gly Glu Ser Arg Asn Leu Ser Gln Met Leu Ser Gln Lys Leu Lys His Thr Gln Glu Arg Asn Pro Ile Val Arg Trp Tyr Lys Ser Phe Met Tyr Phe Leu Leu Asp Asn Trp Gln Arg Val Trp Val Leu Leu Trp Ile Gly Ile Met Ala Gly Leu Phe Thr Trp Lys Tyr Ile Gln Tyr Lys Glu Lys Ala Ala Tyr Lys Val Met Gly Pro Cys Val Cys Phe Ala Lys Gly Ala Ala Glu Thr Leu Lys Leu Asn Met Ala Ile Ile Leu Phe Pro Val Cys Arg Asn Thr Ile Thr Trp Leu Arg Asn Lys Thr Arg Leu Gly Ala Ala Val Pro Phe Asp Asp Asn Leu Asn Phe His Lys Val Ile Ala Val Ala Ile Ala Leu Gly Val Gly Ile His Gly Leu Ser His Leu Thr Cys Asp Phe Pro Arg Leu Leu Asn Ala Ser Glu Glu Glu Tyr Glu Pro Met Lys Tyr Tyr Phe Gly Asp Gln Pro Glu Ser Tyr Trp Trp Phe Ile Lys Gly Val Glu Gly Val Thr Gly Ile Ile Met Val Val Leu Met Ala Ile Ala Phe Thr Leu Ala Thr Pro Trp Phe Arg Arg Asn Arg Val Ser Leu Pro Lys Pro Phe His Lys Leu Thr Gly Xaa Asn Ala Phe Trp Tyr Ser His His Leu Phe Val Ile Val Tyr Thr Leu Phe Ile Val His Gly Glu Lys Leu Tyr Ile Thr Lys Asp Trp Tyr Lys Arg Thr Asp Met Asp Val Leu Leu Thr Ile Pro Ile Ile Leu Tyr Ala Ser Glu Arg Leu Ile Arg Ala Phe Arg Ser Ser Ile Lys Ala Val Lys Ile Leu Lys Val Ala Val Tyr Pro Gly Asn Val Leu Ala Leu His Met Ser Lys Pro Gln Gly Tyr Lys Tyr Lys Ser Gly Gln Tyr Met Phe Val Asn Cys Ala Ala Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His Ile Arg 

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Cys Gln Pro Pro Pro Asn Gly Lys Ser Gly Leu Leu Arg Ala Asp Tyr
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Leu Gln Gly Glu Asn Asn Pro Asn Phe Pro Arg Val Leu Ile Asp Gly
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Pro Tyr Gly Ala Pro Ala Gln Asp Tyr Lys Lys Tyr Glu Val Val Leu
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                                   730
Leu Val Gly Leu Gly Ile Gly Ala Thr Pro Met Ile Ser Ile Val Lys
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Asp Ile Val Asn Asn Met Lys Ala Met Asp Glu Glu Asn Ser Leu
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Glu Asp Gly His Asn Asn Asn Met Ala Pro Asn Ser Ser Pro Asn Ile
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Ala Lys Asn Lys Gly Asn Lys Ser Gly Ser Ala Ser Gly Gly Asn Asn
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Phe Asn Thr Arg Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly
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               805
Ser Phe Asp Trp Phe Lys Gly Ile Met Asn Glu Ala Ala Glu Met Asp
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His Lys Gly Val Ile Glu Met His Asn Tyr Cys Thr Ser Val Tyr Glu
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Glu Gly Asp Ala Arg Ser Ala Leu Ile Thr Met Leu Gln Ser Leu His
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His Ala Lys Asn Gly Val Asp Ile Val Ser Gly Thr Arg Val Lys Ser
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                   87Ò
His Phe Ala Lys Pro Asn Trp Arg Asn Val Tyr Lys Arg Ile Ala Leu
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Asn His Pro Glu Ala Lys Val Gly Val Phe Tyr Cys Gly Ala Pro Ala
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                                                                 96
Gly Leu Pro Arg Pro Pro Gly Ala Gly Ala Gly Ala Ala Ala Gly Gly
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Phe Ala Arg Gly Leu Met Lys Gln Pro Ser Arg Leu Ala Ser Gly Val
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Arg Gln Phe Ala Ser Arg Val Ser Met Lys Val Pro Glu Gly Val Gly
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Gly Met Arg Pro Gly Gly Gly Arg Met Thr Arg Met Gln Ser Ser Ala
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											tgc Cys					384
											gcg Ala 140					432
Arg 145	Asn	Leu	Glu	Pro	Glu 150	Asp	Gly	Ile	Thr	Lys 155	gag Glu	Gln	Leu	Lys	Glu 160	480
											tcg Ser					528
											atg Met					576
											gcg Ala					624
aag Lys	ctg Leu 210	aag Lys	gga Gly	cac His	gcg Ala	gcg Ala 215	acg Thr	tac Tyr	gcg Ala	tcg Ser	ctg Leu 220	atc Ile	atg Met	gag Glu	gag Glu	672
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											ccg Pro					768
											ccg Pro					816
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											ctc Leu 300					912
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Gln	Val	Met	Gly	His 325	Cys	Val	Cys	Val	Ala 330	Lys	Gly	Ala	Ala	Glu 335	Val	1008
Leu	Lys	Leu	Asn 340	Met	Ala	Leu	Ile	Leu 345	Leu	Pro	gtg Val	Cys	Arg 350	Asn	Thr	1056
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Asp	Asn 370	Ile	Asn	Phe	His	Lys 375	Val	Ile	Ala	Ala	acc Thr 380	Ile	Ala	Ala	Ala	1152
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Ile	Asn	Cys	Pro	Ser 405	Asp	Lys	Phe	Met	Ala 410	Thr	Leu	Gly	Pro	Asn 415	Phe	
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gcc Ala	acg Thr 450	cac His	tcc Ser	ttc Phe	cgc Arg	cgg Arg 455	agc	gtc Val	gtc Val	aag Lys	ctg Leu 460	ccg Pro	tcg Ser	ccg Pro	ctg Leu	1392
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acc Thr	agg Arg	gag Glu	tgg Trp 500	tac Tyr	aag Lys	aaa Lys	acg Thr	aca Thr 505	tgg Trp	atg Met	tac Tyr	ctg Leu	ata Ile 510	gtc Val	cca Pro	1536
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aac Asn	tac Tyr 530	cgc Arg	gtg Val	agc Ser	atc Ile	gtc Val 535	aag Lys	gca Ala	gcg Ala	att Ile	tac Tyr 540	cca Pro	gga Gly	aat Asn	gtg Val	1632
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Pro	aag Lys	Val	Leu	Ile 645	Asp	Gly	Pro	Tyr	Gly 650	Ala	Pro	Ala	Gln	Asn 655	Tyr	1968
Lys	aag Lys	Tyr	Asp 660	Ile	Leu	Leu	Leu	Ile 665	Gly	Leu	Gly	Ile	Gly 670	Ala	Thr	2016
Pro	ttc Phe	Ile 675	Ser	Ile	Leu	Lys	Asp 680	Leu	Leu	Asn	Asn	Ile 685	Lys	Ser	Asn	2064
Glu	gag Glu 690	Val	Glu	Ser	Ile	His 695	Gly	Ser	Glu	Ile	Gly 700	Ser	Phe	Lys	Asn	2112
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gaa Glu	ggc Gly	gac Asp 755	gca Ala	agg Arg	Ser	gct Ala	Leu 760	att Ile	gcc Ala	Met	Val	Gln 765	Ser	Leu	Gln	2304
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	Val	Gly	Leu	Arg 85	. •	Leu	Arg	Phe	Leu, 90	_	Lys	Thr	Ser	Gly 95	Gly	
Lys	Glu	Gly	Trp		Ser	Val	Glu	Arg 105		Phe	Asp	Glu	Met 110		Arg	
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			180					Gly 185					190			
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Arg Thr Thr Ser Ser Leu Ala Arg Thr Met Ile Pro Ser Arg Tyr Arg Ser Pro Leu Lys Arg His Val Ser Arg Thr Val Asp Phe Val His Glu Asn Trp Lys Arg Ile Trp Leu Val Ala Leu Trp Leu Ala Val Asn Val Gly Leu Phe Ala Tyr Lys Phe Glu Gln Tyr Glu Arg Arg Ala Ala Phe Gln Val Met Gly His Cys Val Cys Val Ala Lys Gly Ala Ala Glu Val Leu Lys Leu Asn Met Ala Leu Ile Leu Leu Pro Val Cys Arg Asn Thr Leu Thr Thr Leu Arg Ser Thr Ala Leu Ser His Val Ile Pro Phe Asp Asp Asn Ile Asn Phe His Lys Val Ile Ala Ala Thr Ile Ala Ala Ala Thr Ala Val His Thr Leu Ala His Val Thr Cys Asp Phe Pro Arg Leu Ile Asn Cys Pro Ser Asp Lys Phe Met Ala Thr Leu Gly Pro Asn Phe Gly Tyr Arg Gln Pro Thr Tyr Ala Asp Leu Leu Glu Ser Ala Pro Gly 4.30 Val Thr Gly Ile Leu Met Ile Ile Ile Met Ser Phe Ser Phe Thr Leu Ala Thr His Ser Phe Arg Arg Ser Val Val Lys Leu Pro Ser Pro Leu His His Leu Ala Gly Phe Asn Ala Phe Trp Tyr Ala His His Leu Leu Val Leu Ala Tyr Val Leu Leu Val Val His Ser Tyr Phe Ile Phe Leu Thr Arg Glu Trp Tyr Lys Lys Thr Thr Trp Met Tyr Leu Ile Val Pro Val Leu Phe Tyr Ala Cys Glu Arg Thr Ile Arg Lys Val Arg Glu Asn Asn Tyr Arg Val Ser Ile Val Lys Ala Ala Ile Tyr Pro Gly Asn Val Leu Ser Leu His Met Lys Lys Pro Pro Gly Phe Lys Tyr Lys Ser Gly Met Tyr Leu Phe Val Lys Cys Pro Asp Val Ser Pro Phe Glu Trp His Pro Phe Ser Ile Thr Ser Ala Pro Gly Asp Asp Tyr Leu Ser Val His Ile Arg Thr Leu Gly Asp Trp Thr Thr Glu Leu Arg Asn Leu Phe Gly Lys Ala Cys Glu Ala Gln Val Thr Ser Lys Lys Ala Thr Leu Ser Arg Leu Glu Thr Thr Val Val Ala Asp Ala Gln Thr Glu Asp Thr Arg Phe Pro Lys Val Leu Ile Asp Gly Pro Tyr Gly Ala Pro Ala Gln Asn Tyr Lys Lys Tyr Asp Ile Leu Leu Leu Ile Gly Leu Gly Ile Gly Ala Thr Pro Phe Ile Ser Ile Leu Lys Asp Leu Leu Asn Asn Ile Lys Ser Asn Glu Glu Val Glu Ser Ile His Gly Ser Glu Ile Gly Ser Phe Lys Asn Asn Gly Pro Gly Arg Ala Tyr Phe Tyr Trp Val Thr Arg Glu Gln Gly Ser Phe Glu Trp Phe Lys Gly Val Met Asn Asp Val Ala Glu Ser Asp His Asn Asn Ile Ile Glu Met His Asn Tyr Leu Thr Ser Val Tyr Glu

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His Phe Ala Arg Pro Asn Trp Arg Lys Val Phe Ser Asp Leu Ala Asn
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                    790
Ala His Lys Asn Ser Arg Ile Gly Val Phe Tyr Cys Gly Ser Pro Thr
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